

OIFE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/882,694

DATE: 11/13/2001
TIME: 14:56:07

Input Set : A:\Seqlista.txt
Output Set: N:\CRF3\11132001\I882694.raw

#3

4 <110> APPLICANT: Duvick, Jon
5 Maddox, Joyce
6 Gilliam, Jacob
7 Folkerts, Otto
8 Crasta, Oswald R.
10 <120> TITLE OF INVENTION: Compositions and Methods for Fumonisin
11 Detoxification
13 <130> FILE REFERENCE: 35718/208255
15 <140> CURRENT APPLICATION NUMBER: 09/882,694
C--> 16 <141> CURRENT FILING DATE: 2001-06-12 OK
18 <150> PRIOR APPLICATION NUMBER: 09/351,224
19 <151> PRIOR FILING DATE: 1999-07-12
21 <160> NUMBER OF SEQ ID NOS: 11
23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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26 <211> LENGTH: 1691
27 <212> TYPE: DNA
28 <213> ORGANISM: Exophiala spinifera
30 <220> FEATURE:
31 <221> NAME/KEY: misc_feature
32 <222> LOCATION: (0)...(0)
33 <223> OTHER INFORMATION: flavin monooxygenase with intron
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37 ggagccggcc tcagcggcat ctctgctgtg tacaaattgc gaaagctcag actcaacgcc 120
38 aaaatcttcg agggagccc cgattttggc ggcgtctggc actggaaccg ctaccctggc 180
39 gctcgtgttg attcggagac gcccttctac caactgaaca ttcccgaagt atggaaagac 240
40 tggacctggt cttgccgcta tcttgaccag aaagagttgc tgtcatatgt tcaccactgt 300
41 gacaagatcc ggggcttgag aaaagacgtc tacttcggag ctgaggtggt tgatgcgcgg 360
42 tatgccagag atctgggcac ctggactgtc aagacgtcgg ctggccatgt tgcgacggca 420
43 aagtatctca ttctcgctac ggggttgctc cacaggaagc acactcccgc actccccggc 480
44 ctgcgccgatt tcaacgggaa ggtgattcat tcgagtgcct ggcacgaaga cttcgacgca 540
45 gagggccaga gagtcgccgt catcgggtgcc ggggccacaa gcatccagat tgttcaggag 600
46 ttggccaaga aggtgacca ggtaacctg tttatgcgaa ggccgagcta ttgtctgccc 660
47 atgcggcaac gaacgatgga taggaacgaa cagacagcct ggaaggccta ctaccccacg 720
48 ctgtttgaag cgagtcgaaa gtctcggatt ggattcccgg tccaggcacc gtcggttggc 780
49 atctttgaag tcagccccga gcagcgggag gcctatttcg aagagttgtg ggagcgtggg 840
50 gcctttaatt ttcttgcttg ccagtaccga gaagtcattg ttgacaaaaa ggccaaccga 900
51 ctggtctatg acttctgggc caaaaagact cgatctcgta tcgtcaatcc ggcaaagaga 960
52 gatctcatgg ctctcttgga gccgccgtac tggttcggta ccaagcgtc cccactggag 1020
53 agcgactact acgaaatgct ggacaagccg agcgtcgaaa ttgtgaatct agaacaatcg 1080
54 cccattgtgg ctgttacaaa gacaggtgtg ctcttgagtg acggcagcaa gagggaatgc 1140
55 gacacgatcg tgctggcgac gggtttcgac agtttctact gctcgtgagt gtgctcgatc 1200
56 atggctccga gtcgggacgt ttggctgacc ttgaaagatt gacacatatg ggcttgaaaa 1260
57 acaagcacgg agtggacctg aaggaggtgt ggaaagatgg catatctact tatatgggag 1320
58 tcttctctca tggttccccc aatgccttct tcgtcgccac ggctcaagcc ccgaccgtcc 1380
59 tttccaacgg cccaacgata atagaaaccc aagtcgactt gatcgccgat acaattgcaa 1440

ENTERED

P.S

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60 agttggaggc cgagcacgcc acgtccgttg aggcgacgaa atcagcacia gaggcattggt 1500
61 cgattatgat tgccaagatg aacgagcaca ctctgttccc cttgacggat tcgtggtgga 1560
62 ctggaggcaa catccctggg aaagcaacac gtgctttaac cttcataggc gggattgctc 1620
63 tctatgagca gatctgtcaa gagaagggtg ccaattggga tgggtttgat gtgcttcatt 1680
64 ctccctgcta a 1691
66 <210> SEQ ID NO: 2
67 <211> LENGTH: 1638
68 <212> TYPE: DNA
69 <213> ORGANISM: Exophiala spinifera
71 <220> FEATURE:
72 <221> NAME/KEY: misc_feature
73 <222> LOCATION: (0)...(0)
74 <223> OTHER INFORMATION: flavin monooxygenase, fully spliced
76 <400> SEQUENCE: 2
77 atgtcggcca ccagcaactc cagaggcgat tgttccgtcg catgcgacgc catcatcgtt 60
78 ggagccggcc tcagcggcat ctctgctgtg tacaaattgc gaaagctcag actcaacgcc 120
79 aaaatcttcg agggagcccc cgatttttggc ggcgtctggc actggaaccg ctaccctggc 180
80 gctcgtgttg attcggagac gcccttctac caactgaaca ttcccgaagt atggaaagac 240
81 tggacctggt cttgccgcta tcctgaccag aaagagttgc tgcattatgt tcaccactgt 300
82 gacaagatcc ggggcttgag aaaagacgtc tacttcggag ctgaggtggt tgatgcgcgg 360
83 tatgccagag atctgggcac ctggactgtc aagacgtcgg ctggccatgt tgcgacggca 420
84 aagtatctca ttctcgttac ggggttgctc cacaggaagc acactcccgc actccccggc 480
85 ctgcgccgatt tcaacgggaa ggtgattcat tcgagtgcct ggcacgaaga cttcgacgca 540
86 gagggccaga gagtcgccgt catcggtgcc ggggccacaa gcattccagat tgttcaggag 600
87 ttggccaaga aggtgacca ggtaacctatg tttatgcgaa ggccgagcta ttgtctgcc 660
88 atgcggcaac gaacgatgga taggaacgaa cagacagcct ggaaggccta ctaccaccg 720
89 ctgtttgaag cgagtcgaaa gtctcggatt ggattcccgg tccaggcacc gtcggttggc 780
90 atctttgaag tcagccccga gcagcgggag gcctatttcg aagagttgtg ggagcgtggg 840
91 gccctttaatt ttcttgcttg ccagtaccga gaagtcattg ttgacaaaaa ggccaaccga 900
92 ctggtctatg acttctgggc caaaaagact cgatctcgta tcgtcaatcc ggcaaagaga 960
93 gatctcatgg ctctcttgga gccgcctgac tggttcggta ccaagcgtc cccactggag 1020
94 agcgactact acgaaatgct ggacaagccg agcgtcgaaa ttgtgaatct agaacaatcg 1080
95 cccattgttg ctgttacaaa gacaggtgtg ctcttgagtg acggcagcaa gagggaatgc 1140
96 gacacgatcg tgctggcgac gggtttcgac agtttcactg gctcattgac acatatgggc 1200
97 ttgaaaaaca agcacggagt ggacctgaag gaggtgtgga aagatggcat atctacttat 1260
98 atgggagttc tctctcatgg cttccccaat gccttcttcg tcgccacggc tcaagccccg 1320
99 accgtccttt ccaacggccc aacgatcata gaaacccaag tcgacttgat cgccgataca 1380
100 attgcaaagt tggaggccga gcacgccacg tccgttgagg cgacgaaatc agcacaagag 1440
101 gcatggctga ttatgattgc caagatgaac gagcacaactc tgttcccctt gacggattcg 1500
102 tgggtggactg gaggcaacat ccctgggaaa gcaacacgtg ctttaacctt cataggcggg 1560
103 attgctctct atgagcagat ctgtcaagag aaggtggcca attgggatgg gtttgatgtg 1620
104 cttcatgctc cctgctaa 1638
106 <210> SEQ ID NO: 3
107 <211> LENGTH: 545
108 <212> TYPE: PRT
109 <213> ORGANISM: Exophiala spinifera
111 <400> SEQUENCE: 3
112 Met Ser Ala Thr Ser Asn Ser Arg Gly Asp Cys Ser Val Ala Cys Asp
113 1 5 10 15

```

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114 Ala Ile Ile Val Gly Ala Gly Leu Ser Gly Ile Ser Ala Val Tyr Lys
115      20      25      30
116 Leu Arg Lys Leu Arg Leu Asn Ala Lys Ile Phe Glu Gly Ala Pro Asp
117      35      40      45
118 Phe Gly Gly Val Trp His Trp Asn Arg Tyr Pro Gly Ala Arg Val Asp
119      50      55      60
120 Ser Glu Thr Pro Phe Tyr Gln Leu Asn Ile Pro Glu Val Trp Lys Asp
121 65      70      75      80
122 Trp Thr Trp Ser Cys Arg Tyr Pro Asp Gln Lys Glu Leu Leu Ser Tyr
123      85      90      95
124 Val His His Cys Asp Lys Ile Arg Gly Leu Arg Lys Asp Val Tyr Phe
125      100     105     110
126 Gly Ala Glu Val Val Asp Ala Arg Tyr Ala Arg Asp Leu Gly Thr Trp
127      115     120     125
128 Thr Val Lys Thr Ser Ala Gly His Val Ala Thr Ala Lys Tyr Leu Ile
129      130     135     140
130 Leu Ala Thr Gly Leu Leu His Arg Lys His Thr Pro Ala Leu Pro Gly
131 145     150     155     160
132 Leu Ala Asp Phe Asn Gly Lys Val Ile His Ser Ser Ala Trp His Glu
133      165     170     175
134 Asp Phe Asp Ala Glu Gly Gln Arg Val Ala Val Ile Gly Ala Gly Ala
135      180     185     190
136 Thr Ser Ile Gln Ile Val Gln Glu Leu Ala Lys Lys Ala Asp Gln Val
137      195     200     205
138 Thr Met Phe Met Arg Arg Pro Ser Tyr Cys Leu Pro Met Arg Gln Arg
139      210     215     220
140 Thr Met Asp Arg Asn Glu Gln Thr Ala Trp Lys Ala Tyr Tyr Pro Thr
141 225     230     235     240
142 Leu Phe Glu Ala Ser Arg Lys Ser Arg Ile Gly Phe Pro Val Gln Ala
143      245     250     255
144 Pro Ser Val Gly Ile Phe Glu Val Ser Pro Glu Gln Arg Glu Ala Tyr
145      260     265     270
146 Phe Glu Glu Leu Trp Glu Arg Gly Ala Phe Asn Phe Leu Ala Cys Gln
147      275     280     285
148 Tyr Arg Glu Val Met Val Asp Lys Lys Ala Asn Arg Leu Val Tyr Asp
149      290     295     300
150 Phe Trp Ala Lys Lys Thr Arg Ser Arg Ile Val Asn Pro Ala Lys Arg
151 305     310     315     320
152 Asp Leu Met Ala Pro Leu Glu Pro Pro Tyr Trp Phe Gly Thr Lys Arg
153      325     330     335
154 Ser Pro Leu Glu Ser Asp Tyr Tyr Glu Met Leu Asp Lys Pro Ser Val
155      340     345     350
156 Glu Ile Val Asn Leu Glu Gln Ser Pro Ile Val Ala Val Thr Lys Thr
157      355     360     365
158 Gly Val Leu Leu Ser Asp Gly Ser Lys Arg Glu Cys Asp Thr Ile Val
159      370     375     380
160 Leu Ala Thr Gly Phe Asp Ser Phe Thr Gly Ser Leu Thr His Met Gly
161 385     390     395     400
162 Leu Lys Asn Lys His Gly Val Asp Leu Lys Glu Val Trp Lys Asp Gly

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163           405           410           415
164 Ile Ser Thr Tyr Met Gly Val Phe Ser His Gly Phe Pro Asn Ala Phe
165           420           425           430
166 Phe Val Ala Thr Ala Gln Ala Pro Thr Val Leu Ser Asn Gly Pro Thr
167           435           440           445
168 Ile Ile Glu Thr Gln Val Asp Leu Ile Ala Asp Thr Ile Ala Lys Leu
169           450           455           460
170 Glu Ala Glu His Ala Thr Ser Val Glu Ala Thr Lys Ser Ala Gln Glu
171 465           470           475           480
172 Ala Trp Ser Ile Met Ile Ala Lys Met Asn Glu His Thr Leu Phe Pro
173           485           490           495
174 Leu Thr Asp Ser Trp Trp Thr Gly Gly Asn Ile Pro Gly Lys Ala Thr
175           500           505           510
176 Arg Ala Leu Thr Phe Ile Gly Gly Ile Ala Leu Tyr Glu Gln Ile Cys
177           515           520           525
178 Gln Glu Lys Val Ala Asn Trp Asp Gly Phe Asp Val Leu His Ala Pro
179           530           535           540
180 Cys
181 545
184 <210> SEQ ID NO: 4
185 <211> LENGTH: 1464
186 <212> TYPE: DNA
187 <213> ORGANISM: Exophiala spinifera
189 <220> FEATURE:
190 <221> NAME/KEY: misc_feature
191 <222> LOCATION: (0)...(0)
192 <223> OTHER INFORMATION: aldehyde dehydrogenase, fully spliced cDNA
194 <400> SEQUENCE: 4
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196 tccaaggggt ccgagagatt aacgctcacg aaccctgtgg acgaatccac cgttgccact 120
197 gatgttcacg tggccaacgc ggccgatgtc gacagtgcag tagccgcttc ggtgcaggcg 180
198 gtcaaaaagg gcccatggaa gaagttcaca ggtgcacaac gcgcggcgtg catgcttaag 240
199 ttcgcggacc tcgccgagaa gaacgccgag aagctcgctc gtctggagtc gctgccacc 300
200 ggtagaccgg tgtcgatgat cactcatttc gacattccaa acatgggtctc cgtgttttcgc 360
201 tactatgcag gctgggccga caagatcgcc ggaaagacct ttcccagagga caacggcaag 420
202 ccgaattggc gttacgagcc gatgggggtg tgtgctggtg ttgccagctg gaacgcgact 480
203 tttctttaag tcggctggaa gatagccccc gccctcgccg ccggctgctc cttcatcttc 540
204 aaagcctcgg agaaatcccc gctgggcggt ctgggcctcg ctctctcttt cgcagaagcc 600
205 ggattccctc ctggagtcgt gcagttcctc actggagcac gagtgcgggg tgaagcattg 660
206 gcgtcgcaca tggacattgc gaagatcagc ttcacaagat ctgtcggcgg tggccgcgcc 720
207 gtcaagcaag caacactcaa gtccaacatg aagcgcgtca ctctagaact gggggaaaag 780
208 ccaaccatcg tcttcaacga agctcctctc gaacggcagt cgggggaatc ggcaaaggat 840
209 ttctcaaaat tcgggcaaat ttgggtcccc ccctcctggt tgctagtgcg atggggaaat 900
210 ttagcggaga aattccatgg agtccgtcat ggctcatttg gaggtgtca gagatggctt 960
211 ggccagaacc cattggaacc caagaggacg catggtccct tcgtcgacaa gtcccagtac 1020
212 gacagagtct tgggtaacat tgacgttggc aaggataccg cgcagctcct cactggcgtt 1080
213 ggtagaaagg gcgacaaggg attcgcgatt gaaccgacga tatttgtcaa tcccaaacca 1140
214 ggcagcaaaa tttggtttga ggagatcttt ggccccgtct tgtccattaa gacgttcaag 1200
215 acggaagaag aggccattga gattgccaat gacacgactt atgggctagc ctcggtcatt 1260

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216 tataacaaat ctctcaacag gggctctccgt gtctcgtcgg cgctcgagac cggtaggcgtc 1320
217 tcgatcaact tcccctttat ccccgagaca caaactccgt ttggcgcat gaaacaatcg 1380
218 ggctcaggca gagagctagg cgaagaaggg ctcaaggcgt acttgagacc caagaccatt 1440
219 aatatccacg tcaacataga gtga 1464
221 <210> SEQ ID NO: 5
222 <211> LENGTH: 487
223 <212> TYPE: PRT
224 <213> ORGANISM: Exophiala spinifera
226 <400> SEQUENCE: 5
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228 1 5 10 15
229 Glu Phe Val Ser Ser Lys Gly Ser Glu Arg Leu Thr Leu Thr Asn Pro
230 20 25 30
231 Trp Asp Glu Ser Thr Val Ala Thr Asp Val His Val Ala Asn Ala Ala
232 35 40 45
233 Asp Val Asp Ser Ala Val Ala Ala Ser Val Gln Ala Val Lys Lys Gly
234 50 55 60
235 Pro Trp Lys Lys Phe Thr Gly Ala Gln Arg Ala Ala Cys Met Leu Lys
236 65 70 75 80
237 Phe Ala Asp Leu Ala Glu Lys Asn Ala Glu Lys Leu Ala Arg Leu Glu
238 85 90 95
239 Ser Leu Pro Thr Gly Arg Pro Val Ser Met Ile Thr His Phe Asp Ile
240 100 105 110
241 Pro Asn Met Val Ser Val Phe Arg Tyr Tyr Ala Gly Trp Ala Asp Lys
242 115 120 125
243 Ile Ala Gly Lys Thr Phe Pro Glu Asp Asn Gly Lys Pro Asn Trp Arg
244 130 135 140
245 Tyr Glu Pro Met Gly Val Cys Ala Gly Ile Ala Ser Trp Asn Ala Thr
246 145 150 155 160
247 Phe Leu Tyr Val Gly Trp Lys Ile Ala Pro Ala Leu Ala Ala Gly Cys
248 165 170 175
249 Ser Phe Ile Phe Lys Ala Ser Glu Lys Ser Pro Leu Gly Val Leu Gly
250 180 185 190
251 Leu Ala Pro Leu Phe Ala Glu Ala Gly Phe Pro Pro Gly Val Val Gln
252 195 200 205
253 Phe Leu Thr Gly Ala Arg Val Thr Gly Glu Ala Leu Ala Ser His Met
254 210 215 220
255 Asp Ile Ala Lys Ile Ser Phe Thr Arg Ser Val Gly Gly Gly Arg Ala
256 225 230 235 240
257 Val Lys Gln Ala Thr Leu Lys Ser Asn Met Lys Arg Val Thr Leu Glu
258 245 250 255
259 Leu Gly Glu Lys Pro Thr Ile Val Phe Asn Glu Ala Pro Leu Glu Arg
260 260 265 270
261 Gln Ser Gly Glu Ser Ala Lys Asp Phe Ser Lys Phe Gly Gln Ile Trp
262 275 280 285
263 Val Pro Pro Ser Cys Leu Leu Val Gln Trp Gly Asn Leu Ala Glu Lys
264 290 295 300
265 Phe His Gly Val Arg His Gly Ser Phe Gly Gly Cys Gln Arg Trp Leu
266 305 310 315 320

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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DATE: 11/13/2001

TIME: 14:56:08

Input Set : A:\Seqlista.txt

Output Set: N:\CRF3\11132001\I882694.raw

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:630 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11